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1: CAA54576. N2042 [Saccharomy...[gi:496725]

BLink, Domains, Links

LOCUS CAA54576 661 aa linear PLN 24-MAY-1995
DEFINITION N2042 [Saccharomyces cerevisiae].
ACCESSION CAA54576
VERSION CAA54576.1 GI:496725
DBSOURCE embl locus SCN201952, accession X77395.1
KEYWORDS
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1
AUTHORS Verhasselt,P., Aert,R., Voet,M. and Volckaert,G.
TITLE Twelve open reading frames revealed in the 23.6 kb segment flanking
the centromere on the Saccharomyces cerevisiae chromosome XIV right
arm
JOURNAL Yeast 10 (10), 1355-1361 (1994)
MEDLINE 95208356
PUBMED 7900425
REFERENCE 2 (residues 1 to 661)
AUTHORS Volckaert,G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1994) G. Volckaert, Laboratory of Gene
Technology, Catholic University of Leuven, W. Decrooylaan 42, 3001
Leuven, BELGIUM
FEATURES Location/Qualifiers
source 1..661
/organism="Saccharomyces cerevisiae"
/strain="FY1679"
/db_xref="taxon:4932"
/chromosome="XIV"
/map="centromeric region (right arm)"
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/clone_lib="B. Dujon (Paris)"
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CDS 1..661
/gene="N2042"
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/db_xref="GOA:P40345"
/db_xref="SGD:S0005291"
/db_xref="SWISS-PROT:P40345"
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61 dfdrkrkdng rkrwrdsrrl ifilgaflgv 1lpfsfgayh vhnsdsdlfd nfvnfdslkv
121 ylldwkdvip qgissfiddi qagnystssl ddlsenfavg kqlldynie akhpvvmpg
181 vistgieswg vigddecoss ahfrkrlwgs fymlrtmvmd kvcwlkhvml dpetgldppn
241 ftlraaqgfe stdyfiagyw iwnkvfqnlq vigyepnkmt saaydwrlay ldllerdrayf
301 tklikeqielf hqlsgekvcl ighsmgsqii fyfmkwveae gplygnnggrg wvnehidsfi
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421 geeviwgdmk sssedalnnn tdtynfnfirf erntsdafnk nltmkdainm tisispewlq
481 rrvheqysfg yskneelrk nelhhkhwsn pmevplpeap hmkiyciygv nnpterayvy
541 keeddssaln ltidyeskqp vfltegdgtv plvahsmchik waqgaspynp aginvtivem
601 khqpdrrfdi ggaksaeahvd ilgsaelndy ilkiasngnd lveprqlsnl sqwvsqmpfp
661 m

//

Sep 16 2003 13:15:10

DNA is known in yeast

LOCUS SCN201952 23901 bp DNA linear PLN 24-MAY-1995
DEFINITION S.cerevisiae N2019, N2021, N2023, N2025, N2027, N2031, N2048 and N2050 genes.
ACCESSION X77395
VERSION X77395.1 GI:496717
KEYWORDS mitochondrial citrate synthase; PRP2 gene; RNA polymerase III; RNA-dependent ATPase; rpc34 gene; tau34 protein; tRNA-Asn; tRNA-Pro; uridine kinase; URK1 gene; yun34 gene.
SOURCE Saccharomyces cerevisiae.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 23901)
AUTHORS Verhasselt,P., Aert,R., Voet,M. and Volckaert,G.
TITLE Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right arm
JOURNAL Yeast 10 (10), 1355-1361 (1994)
REFERENCE 2 (bases 1 to 23901)
AUTHORS Volckaert,G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1994) G. Volckaert, Laboratory of Gene Technology, Catholic University of Leuven, W. Decrooylaan 42, 3001 Leuven, BELGIUM

Query Match 100.0%; Score 1986; DB 8; Length 23901;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1986; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGCACACTGTTCGAAGAAATGTCCAGAACCAAAAGAGTGATTCTGATGAAAACAAT 60
Db 11755 ATGGGCACACTGTTCGAAGAAATGTCCAGAACCAAAAGAGTGATTCTGATGAAAACAAT 11814

Qy 61 AAAGGGGGTCTGTTCATAACAGCGAGAGAGCAGAAACCACATTCATCATCACAGGGGA 120
Db 11815 AAAGGGGGTCTGTTCATAACAGCGAGAGAGCAGAAACCACATTCATCATCACAGGGGA 11874

Qy 121 TTAGGCCATAAGAGAAGAAGGGTATTAGTGGCAGTGCAAAAGAAATGAGCGTGGCAA 180
Db 11875 TTAGGCCATAAGAGAAGAAGGGTATTAGTGGCAGTGCAAAAGAAATGAGCGTGGCAA 11934

Qy 181 GATTCGACAGGAAAGAGACGGAACGGTAGAAACGTTGGAGAGATTCCAGAAGACTG 240
Db 11935 GATTCGACAGGAAAGAGACGGAACGGTAGAAACGTTGGAGAGATTCCAGAAGACTG 11994

Qy 241 ATTTTCATTCTTGGTGCATTCTTAGGTGTACTTTGCCGTTAGCTTGGCGCTTATCAT 300
Db 11995 ATTTTCATTCTTGGTGCATTCTTAGGTGTACTTTGCCGTTAGCTTGGCGCTTATCAT 12054

Qy 301 GTTCATAATAGCGATAGCGACTTGTGTTGACAACTTGTAAATTGATTCACTTAAAGTG 360
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Qy 361 TATTTGGATGATTGGAAAGATGTTCTCCCACAAGGTATAAGTCGTTATTGATGATATT 420
Db 12115 TATTTGGATGATTGGAAAGATGTTCTCCCACAAGGTATAAGTCGTTATTGATGATATT 12174

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Qy	541	GTCATTCTACGGATTGAAAGCTGGGAGTTATTGGAGACGATGAGTGCATAGTTCT	600
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Qy	601	GCGCATTTCGTAAACGGCTGTGGGAAGTTTACATGCTGAGAACAAATGGTATGGAT	660
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Qy	661	AAAGTTGTTGGTGAAACATGTAATGTTAGATCCTGAAACAGGTCTGGACCCACCGAAC	720
Db	12415	AAAGTTGTTGGTGAAACATGTAATGTTAGATCCTGAAACAGGTCTGGACCCACCGAAC	12474
Qy	721	TTTACGCTACGTGCAGCACAGGGCTTCGAATCAACTGATTATTCATCGCAGGGTATTGG	780
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Qy	781	ATTGGAACAAAGTTCCAAAATCTGGAGTAATTGGCTATGAACCCAATAAAATGACG	840
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Db	12655	ACGAAGCTAAAGGAACAAATCGAACTGTTCATCAATTGAGTGGTAAAAAGTTGTTA	12714
Qy	961	ATTGGACATTCTATGGGTCTCAGATTATCTTACTTTATGAAATGGTCGAGGCTGAA	1020
Db	12715	ATTGGACATTCTATGGGTCTCAGATTATCTTACTTTATGAAATGGTCGAGGCTGAA	12774
Qy	1021	GGCCCTTTACGGTAATGGTGGCTGGCTGGTTACGAACACATAGATTCAATTCTATT	1080
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Qy	1081	AATGCAGCAGGGACGCTCTGGCGCTCAAAGGCAGTCCAGCTAATTAGTGGTGAA	1140
Db	12835	AATGCAGCAGGGACGCTCTGGCGCTCAAAGGCAGTCCAGCTAATTAGTGGTGAA	12894
Qy	1141	ATGAAAGATACCATTCAATTAAATACGTTAGCCATGTATGGTTGGAAAAGTCTTCTCA	1200
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Qy	1201	AGAATTGAGAGAGTAAAATGTTACAAACGTGGGTGGTACCATCAATGCTACCAAAG	1260
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Qy	1261	GGAGAAGAGGTCA T GGGGGATATGAAGTCATCTCAGAGGATGCATTGAATAACAAC	1320
Db	13015	GGAGAAGAGGTCA T GGGGGATATGAAGTCATCTCAGAGGATGCATTGAATAACAAC	13074
Qy	1321	ACTGACACATACGGCA A TTCA T CGATTGAAAGGAATCGAGCGATGCTTCAACAAA	1380
Db	13075	ACTGACACATACGGCA A TTCA T CGATTGAAAGGAATCGAGCGATGCTTCAACAAA	13134
Qy	1381	AATTGACAATGAAAGACGCCATTAACATGACATTATCGATATCACCTGAATGGCTCAA	1440
Db	13135	AATTGACAATGAAAGACGCCATTAACATGACATTATCGATATCACCTGAATGGCTCAA	13194
Qy	1441	AGAAGAGTACATGAGCAGTACTCGTCGGCTATTCCAAGAACATGAAGAAGAGTTAAGAAAA	1500
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Db	13495	TGGGCCAGGGTGCTCACCGTACAACCC T GCC G GAATTACGTTACTATTGTGAAATG	13554
Qy	1801	AAACACCAGCCAGATCGATTGATATACGTGGTGGAGCAAAAGCGCCGAACACGTAGAC	1860
Db	13555	AAACACCAGCCAGATCGATTGATATACGTGGTGGAGCAAAAGCGCCGAACACGTAGAC	13614
Qy	1861	ATCCTCGGCAGCGCGGAGTTGAACGATTACATCTGAAAATTGCAAGCGGTAA T GGCGAT	1920
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Qy	1921	CTCGTCGAGCCACGCCAATTGTCTAATTGAGCCAGTGGTTCTCAGATGCCCTCCCA	1980
Db	13675	CTCGTCGAGCCACGCCAATTGTCTAATTGAGCCAGTGGTTCTCAGATGCCCTCCCA	13734
Qy	1981	ATGTAA 1986	
Db	13735	ATGTAA 13740	